<u>RAW SEQUENCE LISTING</u>

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/585,964_

Source: _IFWP_

Date Processed by STIC: _7/25/06_

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IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/585,964

DATE: 07/25/2006
TIME: 15:09:31

Input Set : A:\NEB-236-PUS.ST25.txt
Output Set: N:\CRF4\07252006\J585964.raw

```
   3 <110> APPLICANT: New England Biolabs, Inc.
   4       Guan, Chudi
   5       Kumar, Sanjay
   6       Kucera, Rebecca
   8 <120> TITLE OF INVENTION: Modified DNA Cleavage Enzymes and Methods of Use (as amended
by
   9       ISA)
  11 <130> FILE REFERENCE: NEB-236-PUS
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/585,964
C--> 13 <141> CURRENT FILING DATE: 2006-07-13
  13 <150> PRIOR APPLICATION NUMBER: 60/524,123
  14 <151> PRIOR FILING DATE: 2003-11-21
  16 <150> PRIOR APPLICATION NUMBER: PCT/US04/039288
  17 <151> PRIOR FILING DATE: 2004-11-22
  19 <160> NUMBER OF SEQ ID NOS: 25
  21 <170> SOFTWARE: PatentIn version 3.2
  23 <210> SEQ ID NO: 1
  24 <211> LENGTH: 450
  25 <212> TYPE: DNA
  26 <213> ORGANISM: unknown
  28 <220> FEATURE:
  29 <223> OTHER INFORMATION: enterobacteria phage T7
  31 <400> SEQUENCE: 1
  32 atggcaggtt acggcgctaa aggaatccga aaggttggag cgtttcgctc tggcctagag      60
  34 gacaaggttt caaagcagtt ggaatcaaaa ggtattaaat tcgagtatga agagtggaaa     120
  36 gtgccttatg taattccggc gagcaatcac acttacactc cagacttctt acttccaaac     180
  38 ggtatattcg ttgagacaaa gggtctgtgg gaaagcgatg atagaaagaa gcacttatta     240
  40 attagggagc agcaccccga gctagacatc cgtattgtct tctcaagctc acgtactaag     300
  42 ttatacaaag gttctccaac gtcttatgga gagttctgcg aaaagcatgg tattaagttc     360
  44 gctgataaac tgatacctgc tgagtggata aaggaaccca agaaggaggt cccctttgat     420
  46 agattaaaaa ggaaaggagg aaagaaataa                                       450
  49 <210> SEQ ID NO: 2
  50 <211> LENGTH: 27
  51 <212> TYPE: DNA
  52 <213> ORGANISM: artificial
  54 <220> FEATURE:
  55 <223> OTHER INFORMATION: primer
  57 <400> SEQUENCE: 2
  58 cccgaattca tggcaggtta cggcgct                                          27
  61 <210> SEQ ID NO: 3
  62 <211> LENGTH: 27
  63 <212> TYPE: DNA
  64 <213> ORGANISM: artificial
  66 <220> FEATURE:
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67 <223> OTHER INFORMATION: primer
69 <400> SEQUENCE: 3
70 cccccaagct tatttctttc ctcctttt   27
73 <210> SEQ ID NO: 4
74 <211> LENGTH: 30
75 <212> TYPE: DNA
76 <213> ORGANISM: unknown
78 <220> FEATURE:
79 <223> OTHER INFORMATION: primer
81 <400> SEQUENCE: 4
82 tggaagtaag aagtctggcc actcttcata   30
85 <210> SEQ ID NO: 5
86 <211> LENGTH: 30
87 <212> TYPE: DNA
88 <213> ORGANISM: artificial
90 <220> FEATURE:
91 <223> OTHER INFORMATION: primer
93 <400> SEQUENCE: 5
94 ttcgagtatg aagagtggcc agacttctta   30
97 <210> SEQ ID NO: 6
98 <211> LENGTH: 39
99 <212> TYPE: DNA
100 <213> ORGANISM: unknown
102 <220> FEATURE:
103 <223> OTHER INFORMATION: oligonucleotide
105 <400> SEQUENCE: 6
106 aaagtgcctt atgtaattgc gagcaatcac acttacact   39
109 <210> SEQ ID NO: 7
110 <211> LENGTH: 39
111 <212> TYPE: DNA
112 <213> ORGANISM: unknown
114 <220> FEATURE:
115 <223> OTHER INFORMATION: oligonucleotide
117 <400> SEQUENCE: 7
118 agtgtaagtg tgattgcacg caattacata aggcacttt   39
121 <210> SEQ ID NO: 8
122 <211> LENGTH: 36
123 <212> TYPE: DNA
124 <213> ORGANISM: unknown
126 <220> FEATURE:
127 <223> OTHER INFORMATION: oligonucleotide
129 <400> SEQUENCE: 8
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133 <210> SEQ ID NO: 9
134 <211> LENGTH: 36
135 <212> TYPE: DNA
136 <213> ORGANISM: unknown
138 <220> FEATURE:
139 <223> OTHER INFORMATION: oligonucleotide

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Input Set : A:\NEB-236-PUS.ST25.txt
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141 <400> SEQUENCE: 9
142 agtgtaagtg tgattgctaa ttacataagg cacttt                          36
145 <210> SEQ ID NO: 10
146 <211> LENGTH: 40
147 <212> TYPE: DNA
148 <213> ORGANISM: unknown
150 <220> FEATURE:
151 <223> OTHER INFORMATION: oligonucleotide mixture
154 <220> FEATURE:
155 <221> NAME/KEY: misc_feature
156 <222> LOCATION: (24)..(24)
157 <223> OTHER INFORMATION: n is a, c, g, or t
159 <400> SEQUENCE: 10
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163 <210> SEQ ID NO: 11
164 <211> LENGTH: 40
165 <212> TYPE: DNA
166 <213> ORGANISM: unknown
168 <220> FEATURE:
169 <223> OTHER INFORMATION: oligonucleotide mixture
172 <220> FEATURE:
173 <221> NAME/KEY: misc_feature
174 <222> LOCATION: (17)..(17)
175 <223> OTHER INFORMATION: n is a, c, g, or t
177 <400> SEQUENCE: 11
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181 <210> SEQ ID NO: 12
182 <211> LENGTH: 149
183 <212> TYPE: PRT
184 <213> ORGANISM: unknown
186 <220> FEATURE:
187 <223> OTHER INFORMATION: enterobacteria phage T7
189 <400> SEQUENCE: 12
191 Met Ala Gly Tyr Gly Ala Lys Gly Ile Arg Lys Val Gly Ala Phe Arg
192 1               5                   10                  15
195 Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
196             20                  25                  30
199 Lys Phe Glu Tyr Glu Glu Trp Lys Val Pro Tyr Val Ile Pro Ala Ser
200         35                  40                  45
203 Asn His Thr Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Val
204     50                  55                  60
207 Glu Thr Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu Leu
208 65                  70                  75                  80
211 Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Ile Val Phe Ser Ser
212                 85                  90                  95
215 Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Phe
216                 100                 105                 110
219 Cys Glu Lys His Gly Ile Lys Phe Ala Asp Lys Leu Ile Pro Ala Glu
220                 115                 120                 125
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Input Set : **A:\NEB-236-PUS.ST25.txt**
Output Set: **N:\CRF4\07252006\J585964.raw**

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223 Trp Ile Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Arg Leu Lys Arg
224     130             135             140
227 Lys Gly Gly Lys Lys
228 145
231 <210> SEQ ID NO: 13
232 <211> LENGTH: 151
233 <212> TYPE: PRT
234 <213> ORGANISM: unknown
236 <220> FEATURE:
237 <223> OTHER INFORMATION: yersinia pestis phage phiA1122
239 <400> SEQUENCE: 13
241 Met Ala Gly Thr Tyr Ala Ala Arg Gly Ile Arg Lys Val Gly Thr Phe
242 1           5               10              15
245 Arg Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Gly Lys Gly
246         20              25              30
249 Ile Lys Phe Asp Tyr Glu Leu Trp Lys Ile Pro Tyr Val Val Pro Ala
250         35              40              45
253 Ser Asn His Val Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe
254     50              55              60
257 Ile Glu Thr Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu
258 65              70              75              80
261 Leu Ile Arg Glu Gln Phe Pro Glu Leu Asp Ile Arg Leu Val Phe Ser
262         85              90              95
265 Ser Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu
266         100             105             110
269 Trp Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val
270         115             120             125
273 Glu Trp Leu Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Arg Leu Lys
274     130             135             140
277 Gln Ala Lys Gly Gly Lys Lys
278 145             150
281 <210> SEQ ID NO: 14
282 <211> LENGTH: 153
283 <212> TYPE: PRT
284 <213> ORGANISM: unknown
286 <220> FEATURE:
287 <223> OTHER INFORMATION: bacteriophage phiYe03-12
289 <400> SEQUENCE: 14
291 Met Ala Gly Ala Tyr Ala Ala Arg Gly Val Arg Lys Val Gly Ala Phe
292 1           5               10              15
295 Arg Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly
296         20              25              30
299 Ile Lys Phe Asp Tyr Glu Leu Trp Arg Ile Pro Tyr Val Ile Pro Ala
300         35              40              45
303 Ser Asp His Leu Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe
304     50              55              60
307 Ile Glu Thr Lys Gly Leu Trp Asp Ser Asp Asp Arg Lys Lys His Leu
308 65              70              75              80
311 Leu Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Leu Val Phe Ser
```

```
312                   85                 90                  95
315 Ser Ser Arg Ser Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Ala Glu
316                   100                105                 110
319 Trp Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val
320         115                120                125
323 Glu Trp Leu Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Lys Phe Lys
324     130                  135                140
327 Thr Lys Lys Gly Val Lys Lys Asn Gly
328 145                  150
331 <210> SEQ ID NO: 15
332 <211> LENGTH: 152
333 <212> TYPE: PRT
334 <213> ORGANISM: Bacteriophage T3
336 <400> SEQUENCE: 15
338 Met Ala Gly Ala Tyr Ala Ala Arg Cys Thr Gln Gly Arg Ala Phe Arg
339 1               5                  10                 15
342 Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
343                   20                25                  30
346 Lys Phe Asp Tyr Glu Leu Trp Arg Ile Pro Tyr Val Ile Pro Glu Ser
347         35                 40                 45
350 Asp His Leu Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Ile
351     50                  55                 60
354 Glu Thr Lys Gly Leu Trp Asp Ser Asp Asp Arg Lys Lys His Leu Leu
355 65                  70                 75                  80
358 Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Leu Val Phe Ser Ser
359                   85                 90                  95
362 Ser Arg Ser Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Trp
363                   100                105                 110
366 Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val Ala
367         115                120                125
370 Gly Val Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Lys Phe Lys Thr
371     130                  135                140
374 Lys Lys Gly Val Lys Lys Asn Gly
375 145                  150
378 <210> SEQ ID NO: 16
379 <211> LENGTH: 147
380 <212> TYPE: PRT
381 <213> ORGANISM: unknown
383 <220> FEATURE:
384 <223> OTHER INFORMATION: pseudomonas phage gh-1
386 <400> SEQUENCE: 16
388 Met Ala Tyr Ala Gly Pro Lys Gly Ala Arg Thr Gly Ala Phe Arg Ser
389 1               5                  10                 15
392 Gly Leu Glu Asp Arg Asn Ala Lys His Met Asp Lys Leu Gly Val Lys
393                   20                25                  30
396 Tyr Asp Phe Glu Arg Phe His Ile Asn Tyr Val Val Pro Ala Arg Asp
397         35                 40                 45
400 Ala Lys Tyr Thr Pro Asp Phe Val Leu Ala Asn Gly Ile Ile Ile Glu
401     50                  55                 60
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/25/2006
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; N Pos. 24
Seq#:11; N Pos. 17

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2,3,5

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
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